

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ullrich, Axel  
Risau, Werner  
Millauer, Birgit  
Gazit, Aviv  
Levitzki, Alex
- (ii) TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular  
Endothelial Growth Factor
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Pennie & Edmonds  
(B) STREET: 1155 Avenue of the Americas  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/193,829  
(B) FILING DATE: 09-FEB-1994  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Coruzzi, Laura A.  
(B) REGISTRATION NUMBER: 30,742  
(C) REFERENCE/DOCKET NUMBER: 7683-060
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (212)790-9090  
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5470 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 286..4386



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TATAGGGCGA ATTGGGTACG GGACCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT	60
CGAATTCGGG CCCAGACTGT GTCCCGCAGC CGGGATAACC TGGCTGACCC GATTCCGCGG	120
ACACCGCTGA CAGCCGCGGC TGGAGCCAGG GCGCCGGTGC CCCGCGCTCT CCCCAGTCTT	180
GCGCTGCGGG GGCCATACCG CCTCTGTGAC TTCTTTGCGG GCCAGGGACG GAGAAGGAGT	240
CTGTGCCTGA GAAACTGGGC TCTGTGCCCA GCGCGAGGT GCAGG ATG GAG AGC	294
Met Glu Ser	
1	
AAG GCG CTG CTA GCT GTC GCT CTG TGG TTC TGC GTG GAG ACC CGA GCC	342
Lys Ala Leu Leu Ala Val Ala Leu Trp Phe Cys Val Glu Thr Arg Ala	
5 10 15	
GCC TCT GTG GGT TTG ACT GGC GAT TTT CTC CAT CCC CCC AAG CTC AGC	390
Ala Ser Val Gly Leu Thr Gly Asp Phe Leu His Pro Pro Lys Leu Ser	
20 25 30 35	
ACA CAG AAA GAC ATA CTG ACA ATT TTG GCA AAT ACA ACC CTT CAG ATT	438
Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile	
40 45 50	
ACT TGC AGG GGA CAG CGG GAC CTG GAC TGG CTT TGG CCC AAT GCT CAG	486
Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Ala Gln	
55 60 65	
CGT GAT TCT GAG GAA AGG GTA TTG GTG ACT GAA TGC GGC GGT GGT GAC	534
Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly Gly Gly Asp	
70 75 80	
AGT ATC TTC TGC AAA ACA CTC ACC ATT CCC AGG GTG GTT GGA AAT GAT	582
Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp	
85 90 95	
ACT GGA GCC TAC AAG TGC TCG TAC CGG GAC GTC GAC ATA GCC TCC ACT	630
Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr	
100 105 110 115	
GTT TAT GTC TAT GTT CGA GAT TAC AGA TCA CCA TTC ATC GCC TCT GTC	678
Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val	
120 125 130	
AGT GAC CAG CAT GGC ATC GTG TAC ATC ACC GAG AAC AAG AAC AAA ACT	726
Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr	
135 140 145	
GTG GTG ATC CCC TGC CGA GGG TCG ATT TCA AAC CTC AAT GTG TCT CTT	774
Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn Val Ser Leu	
150 155 160	
TGC GCT AGG TAT CCA GAA AAG AGA TTT GTT CCG GAT GGA AAC AGA ATT	822
Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile	
165 170 175	
TCC TGG GAC AGC GAG ATA GGC TTT ACT CTC CCC AGT TAC ATG ATC AGC	870
Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr Met Ile Ser	
180 185 190 195	

TAT	GCC	GGC	ATG	GTC	TTC	TGT	GAG	GCA	AAG	ATC	AAT	GAT	GAA	ACC	TAT	918
Tyr	Ala	Gly	Met	Val	Phe	Cys	Glu	Ala	Lys	Ile	Asn	Asp	Glu	Thr	Tyr	
				200					205					210		
CAG	TCT	ATC	ATG	TAC	ATA	GTT	GTG	GTT	GTA	GGA	TAT	AGG	ATT	TAT	GAT	966
Gln	Ser	Ile	Met	Tyr	Ile	Val	Val	Val	Val	Gly	Tyr	Arg	Ile	Tyr	Asp	
			215					220					225			
GTG	ATT	CTG	AGC	CCC	CCG	CAT	GAA	ATT	GAG	CTA	TCT	GCC	GGA	GAA	AAA	1014
Val	Ile	Leu	Ser	Pro	Pro	His	Glu	Ile	Glu	Leu	Ser	Ala	Gly	Glu	Lys	
		230					235					240				
CTT	GTC	TTA	AAT	TGT	ACA	GCG	AGA	ACA	GAG	CTC	AAT	GTG	GGG	CTT	GAT	1062
Leu	Val	Leu	Asn	Cys	Thr	Ala	Arg	Thr	Glu	Leu	Asn	Val	Gly	Leu	Asp	
	245					250					255					
TTC	ACC	TGG	CAC	TCT	CCA	CCT	TCA	AAG	TCT	CAT	CAT	AAG	AAG	ATT	GTA	1110
Phe	Thr	Trp	His	Ser	Pro	Pro	Ser	Lys	Ser	His	His	Lys	Lys	Ile	Val	
					265					270					275	
AAC	CGG	GAT	GTG	AAA	CCC	TTT	CCT	GGG	ACT	GTG	GCG	AAG	ATG	TTT	TTG	1158
Asn	Arg	Asp	Val	Lys	Pro	Phe	Pro	Gly	Thr	Val	Ala	Lys	Met	Phe	Leu	
				280				285						290		
AGC	ACC	TTG	ACA	ATA	GAA	AGT	GTG	ACC	AAG	AGT	GAC	CAA	GGG	GAA	TAC	1206
Ser	Thr	Leu	Thr	Ile	Glu	Ser	Val	Thr	Lys	Ser	Asp	Gln	Gly	Glu	Tyr	
			295				300					305				
ACC	TGT	GTA	GCG	TCC	AGT	GGA	CGG	ATG	ATC	AAG	AGA	AAT	AGA	ACA	TTT	1254
Thr	Cys	Val	Ala	Ser	Ser	Gly	Arg	Met	Ile	Lys	Arg	Asn	Arg	Thr	Phe	
		310					315					320				
GTC	CGA	GTT	CAC	ACA	AAG	CCT	TTT	ATT	GCT	TTC	GGT	AGT	GGG	ATG	AAA	1302
Val	Arg	Val	His	Thr	Lys	Pro	Phe	Ile	Ala	Phe	Gly	Ser	Gly	Met	Lys	
	325					330					335					
TCT	TTG	GTG	GAA	GCC	ACA	GTG	GGC	AGT	CAA	GTC	CGA	ATC	CCT	GTG	AAG	1350
Ser	Leu	Val	Glu	Ala	Thr	Val	Gly	Ser	Gln	Val	Arg	Ile	Pro	Val	Lys	
	340				345					350					355	
TAT	CTC	AGT	TAC	CCA	GCT	CCT	GAT	ATC	AAA	TGG	TAC	AGA	AAT	GGA	AGG	1398
Tyr	Leu	Ser	Tyr	Pro	Ala	Pro	Asp	Ile	Lys	Trp	Tyr	Arg	Asn	Gly	Arg	
				360					365					370		
CCC	ATT	GAG	TCC	AAC	TAC	ACA	ATG	ATT	GTT	GGC	GAT	GAA	CTC	ACC	ATC	1446
Pro	Ile	Glu	Ser	Asn	Tyr	Thr	Met	Ile	Val	Gly	Asp	Glu	Leu	Thr	Ile	
			375					380					385			
ATG	GAA	GTG	ACT	GAA	AGA	GAT	GCA	GGA	AAC	TAC	ACG	GTC	ATC	CTC	ACC	1494
Met	Glu	Val	Thr	Glu	Arg	Asp	Ala	Gly	Asn	Tyr	Thr	Val	Ile	Leu	Thr	
		390					395					400				
AAC	CCC	ATT	TCA	ATG	GAG	AAA	CAG	AGC	CAC	ATG	GTC	TCT	CTG	GTT	GTG	1542
Asn	Pro	Ile	Ser	Met	Glu	Lys	Gln	Ser	His	Met	Val	Ser	Leu	Val	Val	
	405					410					415					
AAT	GTC	CCA	CCC	CAG	ATC	GGT	GAG	AAA	GCC	TTG	ATC	TCG	CCT	ATG	GAT	1590
Asn	Val	Pro	Pro	Gln	Ile	Gly	Glu	Lys	Ala	Leu	Ile	Ser	Pro	Met	Asp	
	420				425					430					435	
TCC	TAC	CAG	TAT	GGG	ACC	ATG	CAG	ACA	TTG	ACA	TGC	ACA	GTC	TAC	GCC	1638

Ser	Tyr	Gln	Tyr	Gly	Thr	Met	Gln	Thr	Leu	Thr	Cys	Thr	Val	Tyr	Ala	
				440					445						450	
AAC	CCT	CCC	CTG	CAC	CAC	ATC	CAG	TGG	TAC	TGG	CAG	CTA	GAA	GAA	GCC	1686
Asn	Pro	Pro	Leu	His	His	Ile	Gln	Trp	Tyr	Trp	Gln	Leu	Glu	Glu	Ala	
			455					460					465			
TGC	TCC	TAC	AGA	CCC	GGC	CAA	ACA	AGC	CCG	TAT	GCT	TGT	AAA	GAA	TGG	1734
Cys	Ser	Tyr	Arg	Pro	Gly	Gln	Thr	Ser	Pro	Tyr	Ala	Cys	Lys	Glu	Trp	
		470					475					480				
AGA	CAC	GTG	GAG	GAT	TTC	CAG	GGG	GGA	AAC	AAG	ATC	GAA	GTC	ACC	AAA	1782
Arg	His	Val	Glu	Asp	Phe	Gln	Gly	Gly	Asn	Lys	Ile	Glu	Val	Thr	Lys	
	485					490					495					
AAC	CAA	TAT	GCC	CTG	ATT	GAA	GGA	AAA	AAC	AAA	ACT	GTA	AGT	ACG	CTG	1830
Asn	Gln	Tyr	Ala	Leu	Ile	Glu	Gly	Lys	Asn	Lys	Thr	Val	Ser	Thr	Leu	
500					505					510					515	
GTC	ATC	CAA	GCT	GCC	AAC	GTG	TCA	GCG	TTG	TAC	AAA	TGT	GAA	GCC	ATC	1878
Val	Ile	Gln	Ala	Ala	Asn	Val	Ser	Ala	Leu	Tyr	Lys	Cys	Glu	Ala	Ile	
				520					525					530		
AAC	AAA	GCG	GGA	CGA	GGA	GAG	AGG	GTC	ATC	TCC	TTC	CAT	GTG	ATC	AGG	1926
Asn	Lys	Ala	Gly	Arg	Gly	Glu	Arg	Val	Ile	Ser	Phe	His	Val	Ile	Arg	
			535					540					545			
GGT	CCT	GAA	ATT	ACT	GTG	CAA	CCT	GCT	GCC	CAG	CCA	ACT	GAG	CAG	GAG	1974
Gly	Pro	Glu	Ile	Thr	Val	Gln	Pro	Ala	Ala	Gln	Pro	Thr	Glu	Gln	Glu	
		550					555					560				
AGT	GTG	TCC	CTG	TTG	TGC	ACT	GCA	GAC	AGA	AAT	ACG	TTT	GAG	AAC	CTC	2022
Ser	Val	Ser	Leu	Leu	Cys	Thr	Ala	Asp	Arg	Asn	Thr	Phe	Glu	Asn	Leu	
	565					570					575					
ACG	TGG	TAC	AAG	CTT	GGC	TCA	CAG	GCA	ACA	TCG	GTC	CAC	ATG	GGC	GAA	2070
Thr	Trp	Tyr	Lys	Leu	Gly	Ser	Gln	Ala	Thr	Ser	Val	His	Met	Gly	Glu	
580					585					590					595	
TCA	CTC	ACA	CCA	GTT	TGC	AAG	AAC	TTG	GAT	GCT	CTT	TGG	AAA	CTG	AAT	2118
Ser	Leu	Thr	Pro	Val	Cys	Lys	Asn	Leu	Asp	Ala	Leu	Trp	Lys	Leu	Asn	
				600					605					610		
GGC	ACC	ATG	TTT	TCT	AAC	AGC	ACA	AAT	GAC	ATC	TTG	ATT	GTG	GCA	TTT	2166
Gly	Thr	Met	Phe	Ser	Asn	Ser	Thr	Asn	Asp	Ile	Leu	Ile	Val	Ala	Phe	
			615					620					625			
CAG	AAT	GCC	TCT	CTG	CAG	GAC	CAA	GGC	GAC	TAT	GTT	TGC	TCT	GCT	CAA	2214
Gln	Asn	Ala	Ser	Leu	Gln	Asp	Gln	Gly	Asp	Tyr	Val	Cys	Ser	Ala	Gln	
		630					635					640				
GAT	AAG	AAG	ACC	AAG	AAA	AGA	CAT	TGC	CTG	GTC	AAA	CAG	CTC	ATC	ATC	2262
Asp	Lys	Lys	Thr	Lys	Lys	Arg	His	Cys	Leu	Val	Lys	Gln	Leu	Ile	Ile	
	645					650					655					
CTA	GAG	CGC	ATG	GCA	CCC	ATG	ATC	ACC	GGA	AAT	CTG	GAG	AAT	CAG	ACA	2310
Leu	Glu	Arg	Met	Ala	Pro	Met	Ile	Thr	Gly	Asn	Leu	Glu	Asn	Gln	Thr	
660					665					670					675	
ACA	ACC	ATT	GGC	GAG	ACC	ATT	GAA	GTG	ACT	TGC	CCA	GCA	TCT	GGA	AAT	2358
Thr	Thr	Ile	Gly	Glu	Thr	Ile	Glu	Val	Thr	Cys	Pro	Ala	Ser	Gly	Asn	

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GAA	TTT	GTT	CCC	TAT	AAG	AGC	AAA	GGG	GCA	CGC	TTC	CGC	CAG	GGC	AAG	3126
Glu	Phe	Val	Pro	Tyr	Lys	Ser	Lys	Gly	Ala	Arg	Phe	Arg	Gln	Gly	Lys	
			935					940					945			
GAC	TAC	GTT	GGG	GAG	CTC	TCC	GTG	GAT	CTG	AAA	AGA	CGC	TTG	GAC	AGC	3174
Asp	Tyr	Val	Gly	Glu	Leu	Ser	Val	Asp	Leu	Lys	Arg	Arg	Leu	Asp	Ser	
		950					955					960				
ATC	ACC	AGC	AGC	CAG	AGC	TCT	GCC	AGC	TCA	GGC	TTT	GTT	GAG	GAG	AAA	3222
Ile	Thr	Ser	Ser	Gln	Ser	Ser	Ala	Ser	Ser	Gly	Phe	Val	Glu	Glu	Lys	
	965					970					975					
TCG	CTC	AGT	GAT	GTA	GAG	GAA	GAA	GAA	GCT	TCT	GAA	GAA	CTG	TAC	AAG	3270
Ser	Leu	Ser	Asp	Val	Glu	Glu	Glu	Glu	Ala	Ser	Glu	Glu	Leu	Tyr	Lys	
980					985					990					995	
GAC	TTC	CTG	ACC	TTG	GAG	CAT	CTC	ATC	TGT	TAC	AGC	TTC	CAA	GTG	GCT	3318
Asp	Phe	Leu	Thr	Leu	Glu	His	Leu	Ile	Cys	Tyr	Ser	Phe	Gln	Val	Ala	
				1000					1005					1010		
AAG	GGC	ATG	GAG	TTC	TTG	GCA	TCA	AGG	AAG	TGT	ATC	CAC	AGG	GAC	CTG	3366
Lys	Gly	Met	Glu	Phe	Leu	Ala	Ser	Arg	Lys	Cys	Ile	His	Arg	Asp	Leu	
			1015					1020					1025			
GCA	GCA	CGA	AAC	ATT	CTC	CTA	TCG	GAG	AAG	AAT	GTG	GTT	AAG	ATC	TGT	3414
Ala	Ala	Arg	Asn	Ile	Leu	Leu	Ser	Glu	Lys	Asn	Val	Val	Lys	Ile	Cys	
		1030					1035					1040				
GAC	TTC	GGC	TTG	GCC	CGG	GAC	ATT	TAT	AAA	GAC	CCG	GAT	TAT	GTC	AGA	3462
Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Tyr	Lys	Asp	Pro	Asp	Tyr	Val	Arg	
	1045					1050					1055					
AAA	GGA	GAT	GCC	CGA	CTC	CCT	TTG	AAG	TGG	ATG	GCC	CCG	GAA	ACC	ATT	3510
Lys	Gly	Asp	Ala	Arg	Leu	Pro	Leu	Lys	Trp	Met	Ala	Pro	Glu	Thr	Ile	
1060					1065					1070					1075	
TTT	GAC	AGA	GTA	TAC	ACA	ATT	CAG	AGC	GAT	GTG	TGG	TCT	TTC	GGT	GTG	3558
Phe	Asp	Arg	Val	Tyr	Thr	Ile	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	
				1080					1085					1090		
TTG	CTC	TGG	GAA	ATA	TTT	TCC	TTA	GGT	GCC	TCC	CCA	TAC	CCT	GGG	GTC	3606
Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu	Gly	Ala	Ser	Pro	Tyr	Pro	Gly	Val	
			1095					1100					1105			
AAG	ATT	GAT	GAA	GAA	TTT	TGT	AGG	AGA	TTG	AAA	GAA	GGA	ACT	AGA	ATG	3654
Lys	Ile	Asp	Glu	Glu	Phe	Cys	Arg	Arg	Leu	Lys	Glu	Gly	Thr	Arg	Met	
		1110					1115					1120				
CGG	GCT	CCT	GAC	TAC	ACT	ACC	CCA	GAA	ATG	TAC	CAG	ACC	ATG	CTG	GAC	3702
Arg	Ala	Pro	Asp	Tyr	Thr	Thr	Pro	Glu	Met	Tyr	Gln	Thr	Met	Leu	Asp	
	1125					1130					1135					
TGC	TGG	CAT	GAG	GAC	CCC	AAC	CAG	AGA	CCC	TCG	TTT	TCA	GAG	TTG	GTG	3750
Cys	Trp	His	Glu	Asp	Pro	Asn	Gln	Arg	Pro	Ser	Phe	Ser	Glu	Leu	Val	
1140					1145					1150					1155	
GAG	CAT	TTG	GGA	AAC	CTC	CTG	CAA	GCA	AAT	GCG	CAG	CAG	GAT	GGC	AAA	3798
Glu	His	Leu	Gly	Asn	Leu	Leu	Gln	Ala	Asn	Ala	Gln	Gln	Asp	Gly	Lys	
				1160					1165				1170			
GAC	TAT	ATT	GTT	CTT	CCA	ATG	TCA	GAG	ACA	CTG	AGC	ATG	GAA	GAG	GAT	3846

Asp Tyr Ile Val Leu Pro Met Ser Glu Thr Leu Ser Met Glu Glu Asp	
1175 1180 1185	
TCT GGA CTC TCC CTG CCT ACC TCA CCT GTT TCC TGT ATG GAG GAA GAG	3894
Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met Glu Glu Glu	
1190 1195 1200	
GAA GTG TGC GAC CCC AAA TTC CAT TAT GAC AAC ACA GCA GGA ATC AGT	3942
Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala Gly Ile Ser	
1205 1210 1215	
CAT TAT CTC CAG AAC AGT AAG CGA AAG AGC CGG CCA GTG AGT GTA AAA	3990
His Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg Pro Val Ser Val Lys	
1220 1225 1230 1235	
ACA TTT GAA GAT ATC CCA TTG GAG GAA CCA GAA GTA AAA GTG ATC CCA	4038
Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu Val Lys Val Ile Pro	
1240 1245 1250	
GAT GAC AGC CAG ACA GAC AGT GGG ATG GTC CTT GCA TCA GAA GAG CTG	4086
Asp Asp Ser Gln Thr Asp Ser Gly Met Val Leu Ala Ser Glu Glu Leu	
1255 1260 1265	
AAA ACT CTG GAA GAC AGG AAC AAA TTA TCT CCA TCT TTT GGT GGA ATG	4134
Lys Thr Leu Glu Asp Arg Asn Lys Leu Ser Pro Ser Phe Gly Gly Met	
1270 1275 1280	
ATG CCC AGT AAA AGC AGG GAG TCT GTG GCC TCG GAA GGC TCC AAC CAG	4182
Met Pro Ser Lys Ser Arg Glu Ser Val Ala Ser Glu Gly Ser Asn Gln	
1285 1290 1295	
ACC AGT GGC TAC CAG TCT GGG TAT CAC TCA GAT GAC ACA GAC ACC ACC	4230
Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp Asp Thr Asp Thr Thr	
1300 1305 1310 1315	
GTG TAC TCC AGC GAC GAG GCA GGA CTT TTA AAG ATG GTG GAT GCT GCA	4278
Val Tyr Ser Ser Asp Glu Ala Gly Leu Leu Lys Met Val Asp Ala Ala	
1320 1325 1330	
GTT CAC GCT GAC TCA GGG ACC ACA CTG CAG CTC ACC TCC TGT TTA AAT	4326
Val His Ala Asp Ser Gly Thr Thr Leu Gln Leu Thr Ser Cys Leu Asn	
1335 1340 1345	
GGA AGT GGT CCT GTC CCG GCT CCG CCC CCA ACT CCT GGA AAT CAC GAG	4374
Gly Ser Gly Pro Val Pro Ala Pro Pro Pro Thr Pro Gly Asn His Glu	
1350 1355 1360	
AGA GGT GCT GCT TAGATTTTCA AGTGTGTGTTT TTTCCACCAC CCGGAAGTAG	4426
Arg Gly Ala Ala	
1365	
CCACATTTGA TTTTCATTTT TGGAGGAGGG ACCTCAGACT GCAAGGAGCT TGTCTCAGG	4486
GCATTTCCAG AGAAGATGCC CATGACCCAA GAATGTGTTG ACTCTACTCT CTTTTCATT	4546
CATTTAAAAG TCCTATATAA TGTGCCCTGC TGTGGTCTCA CTACCAGTTA AAGCAAAAGA	4606
CTTTCAAACA CGTGGACTCT GTCCTCCAAG AAGTGGCAAC GGCACCTCTG TGAAACTGGA	4666
TCGAATGGGC AATGCTTTGT GTGTTGAGGA TGGGTGAGAT GTCCCAGGGC CGAGTCTGTC	4726

TACCTTGGAG GCTTTGTGGA GGATGCGGGC TATGAGCCAA GTGTTAAGTG TGGGATGTGG	4786
ACTGGGAGGA AGGAAGGCGC AAGTCGCTCG GAGAGCGGTT GGAGCCTGCA GATGCATTGT	4846
GCTGGCTCTG GTGGAGGTGG GCTTGTGGCC TGTCAGGAAA CGCAAAGGCG GCCGGCAGGG	4906
TTTGGTTTTG GAAGGTTTGC GTGCTCTTCA CAGTCGGGTT ACAGGCGAGT TCCCTGTGGC	4966
GTTTCCTACT CCTAATGAGA GTTCCTTCCG GACTCTTACG TGTCTCCTGG CCTGGCCCCA	5026
GGAAGGAAAT GATGCAGCTT GCTCCTTCCT CATCTCTCAG GCTGTGCCTT AATTCAGAAC	5086
ACCAAAAGAG AGGAACGTCG GCAGAGGCTC CTGACGGGGC CGAAGAATTG TGAGAACAGA	5146
ACAGAAACTC AGGGTTTCTG CTGGGTGGAG ACCCACGTGG CGCCCTGGTG GCAGGTCTGA	5206
GGGTTCTCTG TCAAGTGGCG GTAAAGGCTC AGGCTGGTGT TCTTCCTCTA TCTCCACTCC	5266
TGTCAGGCCC CCAAGTCCTC AGTATTTTAG CTTTGTGGCT TCCTGATGGC AGAAAAATCT	5326
TAATTGGTTG GTTTGCTCTC CAGATAATCA CTAGCCAGAT TTCGAAATTA CTTTTTAGCC	5386
GAGGTTATGA TAACATCTAC TGTATCCTTT AGAATTTTAA CCTATAAAAC TATGTCTACT	5446
GGTTTCTGCC TGTGTGCTTA TGTT	5470

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1367 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Ser	Lys	Ala	Leu	Leu	Ala	Val	Ala	Leu	Trp	Phe	Cys	Val	Glu
1				5					10					15	
Thr	Arg	Ala	Ala	Ser	Val	Gly	Leu	Thr	Gly	Asp	Phe	Leu	His	Pro	Pro
		20						25					30		
Lys	Leu	Ser	Thr	Gln	Lys	Asp	Ile	Leu	Thr	Ile	Leu	Ala	Asn	Thr	Thr
		35					40					45			
Leu	Gln	Ile	Thr	Cys	Arg	Gly	Gln	Arg	Asp	Leu	Asp	Trp	Leu	Trp	Pro
	50					55				60					
Asn	Ala	Gln	Arg	Asp	Ser	Glu	Glu	Arg	Val	Leu	Val	Thr	Glu	Cys	Gly
	65				70				75					80	
Gly	Gly	Asp	Ser	Ile	Phe	Cys	Lys	Thr	Leu	Thr	Ile	Pro	Arg	Val	Val
			85					90						95	
Gly	Asn	Asp	Thr	Gly	Ala	Tyr	Lys	Cys	Ser	Tyr	Arg	Asp	Val	Asp	Ile
		100					105					110			
Ala	Ser	Thr	Val	Tyr	Val	Tyr	Val	Arg	Asp	Tyr	Arg	Ser	Pro	Phe	Ile
		115					120					125			



Ala Ser Val Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys  
130 135 140  
Asn Lys Thr Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn  
145 150 155 160  
Val Ser Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly  
165 170 175  
Asn Arg Ile Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr  
180 185 190  
Met Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp  
195 200 205  
Glu Thr Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg  
210 215 220  
Ile Tyr Asp Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala  
225 230 235 240  
Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val  
245 250 255  
Gly Leu Asp Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys  
260 265 270  
Lys Ile Val Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys  
275 280 285  
Met Phe Leu Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln  
290 295 300  
Gly Glu Tyr Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn  
305 310 315 320  
Arg Thr Phe Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser  
325 330 335  
Gly Met Lys Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile  
340 345 350  
Pro Val Lys Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg  
355 360 365  
Asn Gly Arg Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu  
370 375 380  
Leu Thr Ile Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val  
385 390 395 400  
Ile Leu Thr Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser  
405 410 415  
Leu Val Val Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser  
420 425 430  
Pro Met Asp Ser Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr  
435 440 445  
Val Tyr Ala Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu

450		455		460
Glu Glu Ala Cys Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys				
465		470		475
Lys Glu Trp Arg His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu				
	485		490	495
Val Thr Lys Asn Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val				
	500		505	510
Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys				
	515		520	525
Glu Ala Ile Asn Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His				
	530		535	540
Val Ile Arg Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr				
	545		550	555
Glu Gln Glu Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe				
	565		570	575
Glu Asn Leu Thr Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His				
	580		585	590
Met Gly Glu Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp				
	595		600	605
Lys Leu Asn Gly Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile				
	610		615	620
Val Ala Phe Gln Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys				
	625		630	635
Ser Ala Gln Asp Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln				
	645		650	655
Leu Ile Ile Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu				
	660		665	670
Asn Gln Thr Thr Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala				
	675		680	685
Ser Gly Asn Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr				
	690		695	700
Leu Val Glu Asp Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu				
	705		710	715
Thr Ile Arg Arg Val Arg Lys Glu Asp Gly Gly Leu Tyr Thr Cys Gln				
	725		730	735
Ala Cys Asn Val Leu Gly Cys Ala Arg Ala Glu Thr Leu Phe Ile Ile				
	740		745	750
Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Val Ile Ile Leu Val Gly				
	755		760	765
Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Val Leu				
	770		775	780

Arg	Thr	Val	Lys	Arg	Ala	Asn	Glu	Gly	Glu	Leu	Lys	Thr	Gly	Tyr	Leu
785					790					795					800
Ser	Ile	Val	Met	Asp	Pro	Asp	Glu	Leu	Pro	Leu	Asp	Glu	Arg	Cys	Glu
				805					810					815	
Arg	Leu	Pro	Tyr	Asp	Ala	Ser	Lys	Trp	Glu	Phe	Pro	Arg	Asp	Arg	Leu
			820					825					830		
Lys	Leu	Gly	Lys	Pro	Leu	Gly	Arg	Gly	Ala	Phe	Gly	Gln	Val	Ile	Glu
		835					840					845			
Ala	Asp	Ala	Phe	Gly	Ile	Asp	Lys	Thr	Ala	Thr	Cys	Lys	Thr	Val	Ala
	850					855					860				
Val	Lys	Met	Leu	Lys	Glu	Gly	Ala	Thr	His	Ser	Glu	His	Arg	Ala	Leu
865					870					875					880
Met	Ser	Glu	Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	His	His	Leu	Asn	Val
				885					890					895	
Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Lys	Pro	Gly	Gly	Pro	Leu	Met	Val
			900					905					910		
Ile	Val	Glu	Phe	Cys	Lys	Phe	Gly	Asn	Leu	Ser	Thr	Tyr	Leu	Arg	Gly
		915					920					925			
Lys	Arg	Asn	Glu	Phe	Val	Pro	Tyr	Lys	Ser	Lys	Gly	Ala	Arg	Phe	Arg
	930					935					940				
Gln	Gly	Lys	Asp	Tyr	Val	Gly	Glu	Leu	Ser	Val	Asp	Leu	Lys	Arg	Arg
945					950					955					960
Leu	Asp	Ser	Ile	Thr	Ser	Ser	Gln	Ser	Ser	Ala	Ser	Ser	Gly	Phe	Val
				965					970					975	
Glu	Glu	Lys	Ser	Leu	Ser	Asp	Val	Glu	Glu	Glu	Glu	Ala	Ser	Glu	Glu
			980					985					990		
Leu	Tyr	Lys	Asp	Phe	Leu	Thr	Leu	Glu	His	Leu	Ile	Cys	Tyr	Ser	Phe
		995					1000					1005			
Gln	Val	Ala	Lys	Gly	Met	Glu	Phe	Leu	Ala	Ser	Arg	Lys	Cys	Ile	His
	1010					1015					1020				
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Leu	Ser	Glu	Lys	Asn	Val	Val
1025					1030					1035					1040
Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Tyr	Lys	Asp	Pro	Asp
				1045					1050					1055	
Tyr	Val	Arg	Lys	Gly	Asp	Ala	Arg	Leu	Pro	Leu	Lys	Trp	Met	Ala	Pro
			1060					1065					1070		
Glu	Thr	Ile	Phe	Asp	Arg	Val	Tyr	Thr	Ile	Gln	Ser	Asp	Val	Trp	Ser
		1075					1080					1085			
Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu	Gly	Ala	Ser	Pro	Tyr
	1090					1095					1100				
Pro	Gly	Val	Lys	Ile	Asp	Glu	Glu	Phe	Cys	Arg	Arg	Leu	Lys	Glu	Gly

1105		1110		1115		1120
Thr Arg Met Arg	Ala Pro Asp Tyr Thr	Thr Pro Glu Met Tyr Gln Thr				
	1125	1130			1135	
Met Leu Asp Cys Trp His Glu Asp	Pro Asn Gln Arg Pro Ser Phe Ser					
	1140	1145		1150		
Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln						
	1155	1160		1165		
Asp Gly Lys Asp Tyr Ile Val Leu Pro Met Ser Glu Thr Leu Ser Met						
	1170	1175		1180		
Glu Glu Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met						
	1185	1190		1195		1200
Glu Glu Glu Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala						
	1205	1210		1215		
Gly Ile Ser His Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg Pro Val						
	1220	1225		1230		
Ser Val Lys Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu Val Lys						
	1235	1240		1245		
Val Ile Pro Asp Asp Ser Gln Thr Asp Ser Gly Met Val Leu Ala Ser						
	1250	1255		1260		
Glu Glu Leu Lys Thr Leu Glu Asp Arg Asn Lys Leu Ser Pro Ser Phe						
	1265	1270		1275		1280
Gly Gly Met Met Pro Ser Lys Ser Arg Glu Ser Val Ala Ser Glu Gly						
	1285	1290		1295		
Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp Asp Thr						
	1300	1305		1310		
Asp Thr Thr Val Tyr Ser Ser Asp Glu Ala Gly Leu Leu Lys Met Val						
	1315	1320		1325		
Asp Ala Ala Val His Ala Asp Ser Gly Thr Thr Leu Gln Leu Thr Ser						
	1330	1335		1340		
Cys Leu Asn Gly Ser Gly Pro Val Pro Ala Pro Pro Pro Thr Pro Gly						
	1345	1350		1355		1360
Asn His Glu Arg Gly Ala Ala						
	1365					

(3) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCATGGATC TTCGTTAA

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(4) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTGTACAAGT ATAAGTAGTA GCCCAGGTAC CAG

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(5) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 806 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Glu	Ser	Lys	Ala	Leu	Leu	Ala	Val	Ala	Leu	Trp	Phe	Cys	Val	Glu	
1				5				10						15		
Thr	Arg	Ala	Ala	Ser	Val	Gly	Leu	Thr	Gly	Asp	Phe	Leu	His	Pro	Pro	
			20				25						30			
Lys	Leu	Ser	Thr	Gln	Lys	Asp	Ile	Leu	Thr	Ile	Leu	Ala	Asn	Thr	Thr	
			35				40					45				
Leu	Gln	Ile	Thr	Cys	Arg	Gly	Gln	Arg	Asp	Leu	Asp	Trp	Leu	Trp	Pro	
	50					55				60						
Asn	Ala	Gln	Arg	Asp	Ser	Glu	Glu	Arg	Val	Leu	Val	Thr	Glu	Cys	Gly	
65					70					75					80	
Gly	Gly	Asp	Ser	Ile	Phe	Cys	Lys	Thr	Leu	Thr	Ile	Pro	Arg	Val	Val	
			85					90						95		
Gly	Asn	Asp	Thr	Gly	Ala	Tyr	Lys	Cys	Ser	Tyr	Arg	Asp	Val	Asp	Ile	
			100				105						110			
Ala	Ser	Thr	Val	Tyr	Val	Tyr	Val	Arg	Asp	Tyr	Arg	Ser	Pro	Phe	Ile	
			115				120						125			

Ala Ser Val Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys  
130 135 140

Asn Lys Thr Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn  
145 150 155 160

Val Ser Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly  
165 170 175

Asn Arg Ile Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr  
180 185 190

Met Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp  
195 200 205

Glu Thr Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg  
210 215 220

Ile Tyr Asp Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala  
225 230 235 240

Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val  
245 250 255

Gly Leu Asp Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys  
260 265 270

Lys Ile Val Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys  
275 280 285

Met Phe Leu Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln  
290 295 300

Gly Glu Tyr Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn  
305 310 315 320

Arg Thr Phe Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser  
325 330 335

Gly Met Lys Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile  
340 345 350

Pro Val Lys Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg  
355 360 365

Asn Gly Arg Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu  
370 375 380

Leu Thr Ile Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val  
385 390 395 400

Ile Leu Thr Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser  
405 410 415

Leu Val Val Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser  
420 425 430

Pro Met Asp Ser Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr  
435 440 445

Val Tyr Ala Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu

450					455					460						
Glu	Glu	Ala	Cys	Ser	Tyr	Arg	Pro	Gly	Gln	Thr	Ser	Pro	Tyr	Ala	Cys	
465					470					475					480	
Lys	Glu	Trp	Arg	His	Val	Glu	Asp	Phe	Gln	Gly	Gly	Asn	Lys	Ile	Glu	
				485					490					495		
Val	Thr	Lys	Asn	Gln	Tyr	Ala	Leu	Ile	Glu	Gly	Lys	Asn	Lys	Thr	Val	
			500					505					510			
Ser	Thr	Leu	Val	Ile	Gln	Ala	Ala	Asn	Val	Ser	Ala	Leu	Tyr	Lys	Cys	
		515					520					525				
Glu	Ala	Ile	Asn	Lys	Ala	Gly	Arg	Gly	Glu	Arg	Val	Ile	Ser	Phe	His	
	530					535					540					
Val	Ile	Arg	Gly	Pro	Glu	Ile	Thr	Val	Gln	Pro	Ala	Ala	Gln	Pro	Thr	
545					550					555					560	
Glu	Gln	Glu	Ser	Val	Ser	Leu	Leu	Cys	Thr	Ala	Asp	Arg	Asn	Thr	Phe	
				565					570					575		
Glu	Asn	Leu	Thr	Trp	Tyr	Lys	Leu	Gly	Ser	Gln	Ala	Thr	Ser	Val	His	
			580					585					590			
Met	Gly	Glu	Ser	Leu	Thr	Pro	Val	Cys	Lys	Asn	Leu	Asp	Ala	Leu	Trp	
		595					600					605				
Lys	Leu	Asn	Gly	Thr	Met	Phe	Ser	Asn	Ser	Thr	Asn	Asp	Ile	Leu	Ile	
	610					615					620					
Val	Ala	Phe	Gln	Asn	Ala	Ser	Leu	Gln	Asp	Gln	Gly	Asp	Tyr	Val	Cys	
625					630					635					640	
Ser	Ala	Gln	Asp	Lys	Lys	Thr	Lys	Lys	Arg	His	Cys	Leu	Val	Lys	Gln	
				645					650					655		
Leu	Ile	Ile	Leu	Glu	Arg	Met	Ala	Pro	Met	Ile	Thr	Gly	Asn	Leu	Glu	
			660					665					670			
Asn	Gln	Thr	Thr	Thr	Ile	Gly	Glu	Thr	Ile	Glu	Val	Thr	Cys	Pro	Ala	
		675					680						685			
Ser	Gly	Asn	Pro	Thr	Pro	His	Ile	Thr	Trp	Phe	Lys	Asp	Asn	Glu	Thr	
	690					695					700					
Leu	Val	Glu	Asp	Ser	Gly	Ile	Val	Leu	Arg	Asp	Gly	Asn	Arg	Asn	Leu	
705					710					715					720	
Thr	Ile	Arg	Arg	Val	Arg	Lys	Glu	Asp	Gly	Gly	Leu	Tyr	Thr	Cys	Gln	
				725					730					735		
Ala	Cys	Asn	Val	Leu	Gly	Cys	Ala	Arg	Ala	Glu	Thr	Leu	Phe	Ile	Ile	
			740					745					750			
Glu	Gly	Ala	Gln	Glu	Lys	Thr	Asn	Leu	Glu	Val	Ile	Ile	Leu	Val	Gly	
		755					760					765				
Thr	Ala	Val	Ile	Ala	Met	Phe	Phe	Trp	Leu	Leu	Leu	Val	Ile	Val	Leu	
	770					775						780				

Arg Thr Val Lys Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu  
785 790 795 800

Ser Ile Val Met Asp Pro

(6) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ile	Leu	Ile	His	Ile	Gly	His	His	Leu	Asn	Val	Val	Asn	Leu	Leu	Gly	1	5	10	15
Ala	Cys	Thr	Lys	Pro	Gly	Gly	Pro	Leu	Met	Val	Ile	Val	Glu	Phe	Cys	20	25	30	
Lys	Phe	Gly	Asn	Leu	Ser	Thr	Tyr	Leu	Arg	Gly	Lys	Arg	Asn	Glu	Phe	35	40	45	
Val	Pro	Tyr	Lys	Ser	Lys	Gly	Ala	Arg	Phe	Arg	Gln	Gly	Lys	Asp	Tyr	50	55	60	
Val	Gly	Glu	Leu	Ser	Val	Asp	Leu	Lys	Arg	Arg	Leu	Asp	Ser	Ile	Thr	65	70	75	80
Ser	Ser	Gln	Ser	Ser	Ala	Ser	Ser	Gly	Phe	Val	Glu	Glu	Lys	Ser	Leu	85	90	95	
Ser	Asp	Val	Glu	Glu	Glu	Glu	Ala	Ser	Glu	Glu	Leu	Tyr	Lys	Asp	Phe	100	105	110	
Leu	Thr	Leu	Glu	His	Leu	Ile	Cys	Tyr	Ser	Phe	Gln	Val	Ala	Lys	Gly	115	120	125	
Met	Glu	Phe	Leu	Ala	Ser	Arg	Lys	Cys	Ile	His	Arg	Asp	Leu	Ala	Ala	130	135	140	
Arg	Asn	Ile	Leu	Leu	Ser	Glu	Lys	Asn	Val	Val	Lys	Ile	Cys	Asp	Phe	145	150	155	160
Gly	Leu	Ala	Arg	Asp	Ile	Tyr	Lys	Asp	Pro	Asp	Tyr	Val	Arg	Lys	Gly	165	170	175	
Asp	Ala	Arg	Leu	180															